

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/023,673

DATE: 01/15/2002

TIME: 18:10:21

Input Set : A:\seq_listing.txt

Output Set: N:\CRF3\01152002\J023673.raw

ENTERED

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4 <110> APPLICANT: Chen, Hong
5      Silos-Santiago, Immaculada
7 <120> TITLE OF INVENTION: NI69, A Novel Nucleoside Transporter
8      Family Member And Uses Therefor
12 <130> FILE REFERENCE: MPI2000-433CP1(M)
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/023,673
C--> 14 <141> CURRENT FILING DATE: 2001-12-17
14 <150> PRIOR APPLICATION NUMBER: 09/712797
15 <151> PRIOR FILING DATE: 2000-11-14
17 <160> NUMBER OF SEQ ID NOS: 3
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 2625
23 <212> TYPE: DNA
24 <213> ORGANISM: Human
26 <220> FEATURE:
27 <221> NAME/KEY: 3'UTR
28 <222> LOCATION: (1)...(52)
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (53)...(1477)
33 <221> NAME/KEY: 5'UTR
34 <222> LOCATION: (1478)...(2625)
36 <400> SEQUENCE: 1
37 gtcgacccac gcgtccgctt agaaggagca caggaaagtc ccagaggctg cc atg ggc 58
38                                     Met Gly
39                                     1
41 tcc gtg ggg agc cag cgc ctt gag gag ccc agc gtg gca ggc aca cca 106
42 Ser Val Gly Ser Gln Arg Leu Glu Glu Pro Ser Val Ala Gly Thr Pro
43      5                                10                                15
45 gac ccg ggc gta gtg atg agc ttc ctg ctg cca tac aac agc ttc atc 154
46 Asp Pro Gly Val Val Met Ser Phe Leu Leu Pro Tyr Asn Ser Phe Ile
47      20                                25                                30
49 acg gac gtg gac tac ctg cat cac aag tac cca ggg acc tcc atc gtg 202
50 Thr Asp Val Asp Tyr Leu His His Lys Tyr Pro Gly Thr Ser Ile Val
51 35                                40                                45                                50
53 ttt qac atg agc ctc acc tac atc ttg gtg gca ctg gca gct gtc ctc 250
54 Phe Asp Met Ser Leu Thr Tyr Ile Leu Val Ala Leu Ala Ala Val Leu
55      55                                60                                65
57 ctg aac aac gtc ctg gtg gag aga ctg acc ctg cac acc agg atc acc 298
58 Leu Asn Asn Val Leu Val Glu Arg Leu Thr Leu His Thr Arg Ile Thr
59      70                                75                                80
61 gca ggc tac ctc tta gcc ttg ggc cct ctc ctt ttt atc agc atc tgc 346
62 Ala Gly Tyr Leu Leu Ala Leu Gly Pro Leu Leu Phe Ile Ser Ile Cys
63      85                                90                                95
65 gac gtg tgg ctg cag ctc ttc tct cgg gac cag gcc tac gcc atc aac 394
66 Asp Val Trp Leu Gln Leu Phe Ser Arg Asp Gln Ala Tyr Ala Ile Asn
67      100                                105                                110

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69	ctg	gcc	gct	gtg	ggc	acc	gtg	gcc	ttc	ggc	tgc	aca	gtg	cag	caa	tcc	442
70	Leu	Ala	Ala	Val	Gly	Thr	Val	Ala	Phe	Gly	Cys	Thr	Val	Gln	Gln	Ser	
71	115				120					125						130	
73	agc	ttc	tac	ggg	tac	acg	gag	atg	ctg	ccc	aag	cgg	tac	acg	cag	ggg	490
74	Ser	Phe	Tyr	Gly	Tyr	Thr	Gly	Met	Leu	Pro	Lys	Arg	Tyr	Thr	Gln	Gly	
75				135						140						145	
77	gtg	atg	acc	ggg	gag	agc	acg	gcg	ggc	gtg	atg	atc	tct	ctg	agc	cgc	538
78	Val	Met	Thr	Gly	Glu	Ser	Thr	Ala	Gly	Val	Met	Ile	Ser	Leu	Ser	Arg	
79				150						155						160	
81	atc	ctc	acg	aag	ctg	ctg	ctg	ccc	gac	gag	cgc	gcc	agc	acg	ctc	atc	586
82	Ile	Leu	Thr	Lys	Leu	Leu	Leu	Pro	Asp	Glu	Arg	Ala	Ser	Thr	Leu	Ile	
83				165						170						175	
85	ttc	ttc	ctg	gtg	tgc	gtg	gcg	ctg	gag	ctg	ctg	tgt	ttc	ctg	ctg	cac	634
86	Phe	Phe	Leu	Val	Ser	Val	Ala	Leu	Glu	Leu	Leu	Cys	Phe	Leu	Leu	His	
87	180									185						190	
89	ctg	tta	gtg	cgg	cgc	agc	cgc	ttc	gtg	ctc	ttc	tat	acc	aca	cgg	cgg	682
90	Leu	Leu	Val	Arg	Arg	Ser	Arg	Phe	Val	Leu	Phe	Tyr	Thr	Thr	Arg	Pro	
91	195						200					205				210	
93	cgt	gac	agc	cac	cgg	ggc	agg	cca	ggc	ctg	ggc	agg	ggc	tat	ggc	tac	730
94	Arg	Asp	Ser	His	Arg	Gly	Arg	Pro	Gly	Leu	Gly	Arg	Gly	Tyr	Gly	Tyr	
95				215						220						225	
97	cgc	gtg	cac	cac	gac	gtt	gtc	gcc	ggg	gac	gtc	cac	ttc	gag	cac	cca	778
98	Arg	Val	His	His	Asp	Val	Val	Ala	Gly	Asp	Val	His	Phe	Glu	His	Pro	
99				230						235						240	
101	gcc	ccg	gcc	ctg	gcc	ccc	aac	gag	tcc	cca	aag	gac	agc	cca	gcc	cac	826
102	Ala	Pro	Ala	Leu	Ala	Pro	Asn	Glu	Ser	Pro	Lys	Asp	Ser	Pro	Ala	His	
103				245						250						255	
105	gag	gtg	acc	ggc	agc	ggc	ggg	gcc	tac	atg	cgc	ttt	gac	gtg	ccg	cgg	874
106	Glu	Val	Thr	Gly	Ser	Gly	Gly	Ala	Tyr	Met	Arg	Phe	Asp	Val	Pro	Arg	
107				260						265						270	
109	cca	agg	gtc	cag	cgc	agc	tgg	ccc	acc	ttc	aga	gcc	ctg	tta	ctg	cac	922
110	Pro	Arg	Val	Gln	Arg	Ser	Trp	Pro	Thr	Phe	Arg	Ala	Leu	Leu	Leu	His	
111	275						280					285				290	
113	cgc	tac	gtg	gtg	gcg	cgg	gtg	atc	tgg	gcc	gac	atg	ctc	tcc	atc	gcc	970
114	Arg	Tyr	Val	Val	Ala	Arg	Val	Ile	Trp	Ala	Asp	Met	Leu	Ser	Ile	Ala	
115				295						300						305	
117	gtg	acc	tac	ttc	atc	acg	ctg	tgc	ctg	ttc	ccc	ggc	ctc	gag	tct	gag	1018
118	Val	Thr	Tyr	Phe	Ile	Thr	Leu	Cys	Leu	Phe	Pro	Gly	Leu	Glu	Ser	Glu	
119				310						315						320	
121	atc	cgc	cac	tgc	atc	ctg	ggc	gag	tgg	ctg	ccc	atc	ctc	atc	atg	gct	1066
122	Ile	Arg	His	Cys	Ile	Leu	Gly	Glu	Trp	Leu	Pro	Ile	Leu	Ile	Met	Ala	
123				325						330						335	
125	gtg	ttc	aac	ctg	tca	gac	ttc	gtg	ggc	aag	atc	ctg	gca	gcc	ctg	ccc	1114
126	Val	Phe	Asn	Leu	Ser	Asp	Phe	Val	Gly	Lys	Ile	Leu	Ala	Ala	Leu	Pro	
127				340						345						350	
129	gtg	gac	tgg	cgg	ggc	acc	cac	ctg	ctg	gcc	tgc	tcc	tgc	ctg	cgt	gtg	1162
130	Val	Asp	Trp	Arg	Gly	Thr	His	Leu	Leu	Ala	Cys	Ser	Cys	Leu	Arg	Val	
131	355						360					365				370	
133	gtc	ttc	atc	ccc	ctc	ttc	atc	ctg	tgc	gtc	tac	ccc	agc	ggc	atg	ccc	1210

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134 Val Phe Ile Pro Leu Phe Ile Leu Cys Val Tyr Pro Ser Gly Met Pro
135          375          380          385
137 gcc ctc cgt cac ccc gcc tgg ccc tgc atc ttc tca ctg ctc atg gcc 1258
138 Ala Leu Arg His Pro Ala Trp Pro Cys Ile Phe Ser Leu Leu Met Gly
139          390          395          400
141 atc agc aac gcc tac ttc gcc agc gtg ccc atg atc ctg gag gca gcc 1306
142 Ile Ser Asn Gly Tyr Phe Gly Ser Val Pro Met Ile Leu Ala Ala Gly
143          405          410          415
145 aaa gtg agc ccc aag cag cgg gag ctg gca ggg aac acc atg acc gtg 1354
146 Lys Val Ser Pro Lys Gln Arg Glu Leu Ala Gly Asn Thr Met Thr Val
147          420          425          430
149 tcc tac atg tca ggg ctg acg ctg ggg tcc gcc gtg gcc tac tgc acc 1402
150 Ser Tyr Met Ser Gly Leu Thr Leu Gly Ser Ala Val Ala Tyr Cys Thr
151 435          440          445          450
153 tac agc ctc acc cgc gac gct cac ggc agc tgc ctg cac gcc tcc acc 1450
154 Tyr Ser Leu Thr Arg Asp Ala His Gly Ser Cys Leu His Ala Ser Thr
155          455          460          465
157 gcc aat ggt tcc atc ctc gca ggc ctc tgagccagcc ccgcccactg 1497
158 Ala Asn Gly Ser Ile Leu Ala Gly Leu
159          470          475
161 ccaggggacgc cgaggggctg accaggggccc ccgagggctg agggcccctc cccgtgcccc 1557
162 acctcagtgc ctgaggggcc ctgagccctcc cccgtgtgcca gcagcccccac tccctcaggg 1617
163 tccagccatg cccaccctg gactgaagtt ctgcaaagtc ctccgaggac cggaacacgt 1677
164 ttctgcgacc cggggtcttg gccagcactg tgtttctggt ttggtctcat acctgcgtct 1737
165 accttcacac tgtgtccagc ggcgccggct ccagcccagc cagcactctg cagggtcaca 1797
166 cgcaccgtgt ccccaaccag gacagcagac acccgccaga gtgtgcgcgc ccagtgaactg 1857
167 caccgccggc ctcatcacc accggcactg atcggggca cgcctggccc agcctccacc 1917
168 agggaccctt cctcatgaac tctggagccc tgagaggaga ggggcagccc cccaccttgt 1977
169 caccctcagg gcttcccctt ctgtcctcat tcttagagac tcttctccc aaacataacg 2037
170 cgttagccat gaaggagtgc gagccctggg tccgaatgga ccgcctgcg gtctgcatca 2097
171 gctctgsga aaccacagca gtgatgccag ctgggcacgt caggacctcc ccacacccc 2157
172 acacgatgcc acaggtcagg ggctgtgccc tgactaggga gccctcccat tgccttctctg 2217
173 gcccgggata gaagagggga ggtaagtctg ggggtacga agccggggcc ccacacctg 2277
174 gctgaagtca gcttgacctt ggtcttgacc ctcatccagc aagggaactg acagacccaa 2337
175 gggtccttgg aacgtaggga ggggctgggg gtcactccag cccgggccc ccagaacacc 2397
176 aggccctgtt gggtagcacc ctgaggtcag gggatcctaa ggggtgcctt ccagagacgg 2457
177 tgtttccagg gggaggaccg ccccgcttc cagatccccg gcccgggctg tgactgccct 2517
178 qtttcacccc tctgtgtccc catccccctg ctgtccacta actgtaccgc accggccatt 2577
179 aaaagatgaa ggcagaccgc tgcaaaaaaa aaaaaaaagg gcgggcgc 2625
181 <210> SEQ ID NO: 2
182 <211> LENGTH: 475
183 <212> TYPE: PRT
184 <213> ORGANISM: Human
186 <400> SEQUENCE: 2
187 Met Gly Ser Val Gly Ser Gln Arg Leu Glu Glu Pro Ser Val Ala Gly
188 1 5 10 15
189 Thr Pro Asp Pro Gly Val Val Met Ser Phe Leu Leu Pro Tyr Asn Ser
190 20 25 30
191 Phe Ile Thr Asp Val Asp Tyr Leu His His Lys Tyr Pro Gly Thr Ser

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192          35          40          45
193 Ile Val Phe Asp Met Ser Leu Thr Tyr Ile Leu Val Ala Leu Ala Ala
194          50          55          60
195 Val Leu Leu Asn Asn Val Leu Val Glu Arg Leu Thr Leu His Thr Arg
196 65          70          75          80
197 Ile Thr Ala Gly Tyr Leu Leu Ala Leu Gly Pro Leu Leu Phe Ile Ser
198          85          90          95
199 Ile Cys Asp Val Trp Leu Gln Leu Phe Ser Arg Asp Gln Ala Tyr Ala
200          100          105          110
201 Ile Asn Leu Ala Ala Val Gly Thr Val Ala Phe Gly Cys Thr Val Gln
202          115          120          125
203 Gln Ser Ser Phe Tyr Gly Tyr Thr Gly Met Leu Pro Lys Arg Tyr Thr
204          130          135          140
205 Gln Gly Val Met Thr Gly Glu Ser Thr Ala Gly Val Met Ile Ser Leu
206 145          150          155          160
207 Ser Arg Ile Leu Thr Lys Leu Leu Leu Pro Asp Glu Arg Ala Ser Thr
208          165          170          175
209 Leu Ile Phe Phe Leu Val Ser Val Ala Leu Glu Leu Leu Cys Phe Leu
210          180          185          190
211 Leu His Leu Leu Val Arg Arg Ser Arg Phe Val Leu Phe Tyr Thr Thr
212          195          200          205
213 Arg Pro Arg Asp Ser His Arg Gly Arg Pro Gly Leu Gly Arg Gly Tyr
214          210          215          220
215 Gly Tyr Arg Val His His Asp Val Val Ala Gly Asp Val His Phe Glu
216 225          230          235          240
217 His Pro Ala Pro Ala Leu Ala Pro Asn Glu Ser Pro Lys Asp Ser Pro
218          245          250          255
219 Ala His Glu Val Thr Gly Ser Gly Gly Ala Tyr Met Arg Phe Asp Val
220          260          265          270
221 Pro Arg Pro Arg Val Gln Arg Ser Trp Pro Thr Phe Arg Ala Leu Leu
222          275          280          285
223 Leu His Arg Tyr Val Val Ala Arg Val Ile Trp Ala Asp Met Leu Ser
224          290          295          300
225 Ile Ala Val Thr Tyr Phe Ile Thr Leu Cys Leu Phe Pro Gly Leu Glu
226 305          310          315          320
227 Ser Glu Ile Arg His Cys Ile Leu Gly Glu Trp Leu Pro Ile Leu Ile
228          325          330          335
229 Met Ala Val Phe Asn Leu Ser Asp Phe Val Gly Lys Ile Leu Ala Ala
230          340          345          350
231 Leu Pro Val Asp Trp Arg Gly Thr His Leu Leu Ala Cys Ser Cys Leu
232          355          360          365
233 Arg Val Val Phe Ile Pro Leu Phe Ile Leu Cys Val Tyr Pro Ser Gly
234          370          375          380
235 Met Pro Ala Leu Arg His Pro Ala Trp Pro Cys Ile Phe Ser Leu Leu
236 385          390          395          400
237 Met Gly Ile Ser Asn Gly Tyr Phe Gly Ser Val Pro Met Ile Leu Ala
238          405          410          415
239 Ala Gly Lys Val Ser Pro Lys Gln Arg Glu Leu Ala Gly Asn Thr Met
240          420          425          430

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```

241 Thr Val Ser Tyr Met Ser Gly Leu Thr Leu Gly Ser Ala Val Ala Tyr
242          435          440          445
243 Cys Thr Tyr Ser Leu Thr Arg Asp Ala His Gly Ser Cys Leu His Ala
244          450          455          460
245 Ser Thr Ala Asn Gly Ser Ile Leu Ala Gly Leu
246 465          470          475
249 <210> SEQ ID NO: 3
250 <211> LENGTH: 1428
251 <212> TYPE: DNA
252 <213> ORGANISM: Human
254 <220> FEATURE:
255 <221> NAME/KEY: CDS
256 <222> LOCATION: (1)...(1428)
258 <400> SEQUENCE: 3
259 atg ggc tcc gtg ggg agc cag cgc ctt gag gag ccc agc gtg gca ggc      48
260 Met Gly Ser Val Gly Ser Gln Arg Leu Glu Glu Pro Ser Val Ala Gly
261 1          5          10          15
263 aca cca gac ccg ggc gta gtg atg agc ttc ctg ctg cca tac aac agc      96
264 Thr Pro Asp Pro Gly Val Val Met Ser Phe Leu Leu Pro Tyr Asn Ser
265          20          25          30
267 ttc atc acg gac gtg gac tac ctg cat cac aag tac cca ggg acc tcc      144
268 Phe Ile Thr Asp Val Asp Tyr Leu His His Lys Tyr Pro Gly Thr Ser
269          35          40          45
271 atc gtg ttt gac atg agc ctc acc tac atc ttg gtg gca ctg gca gct      192
272 Ile Val Phe Asp Met Ser Leu Thr Tyr Ile Leu Val Ala Leu Ala Ala
273          50          55          60
275 gtc ctc ctg aac aac gtc ctg gtg gag aga ctg acc ctg cac acc agg      240
276 Val Leu Leu Asn Asn Val Leu Val Glu Arg Leu Thr Leu His Thr Arg
277 65          70          75          80
279 atc acc gca ggc tac ctc tta gcc ttg ggc cct ctc ctt ttt atc agc      288
280 Ile Thr Ala Gly Tyr Leu Leu Ala Leu Gly Pro Leu Leu Phe Ile Ser
281          85          90          95
283 atc tgc gac gtg tgg ctg cag ctc ttc tct cgg gac cag gcc tac gcc      336
284 Ile Cys Asp Val Trp Leu Gln Leu Phe Ser Arg Asp Gln Ala Tyr Ala
285          100          105          110
287 atc aac ctg gcc gct gtg ggc acc gtg gcc ttc ggc tgc aca gtg cag      384
288 Ile Asn Leu Ala Ala Val Gly Thr Val Ala Phe Gly Cys Thr Val Gln
289          115          120          125
291 caa tcc agc ttc tac ggg tac acg ggg atg ctg ccc aag cgg tac acg      432
292 Gln Ser Ser Phe Tyr Gly Tyr Thr Gly Met Leu Pro Lys Arg Tyr Thr
293          130          135          140
295 cag ggg gtg atg acc ggg gag agc acg gcg ggc gtg atg atc tct ctg      480
296 Gln Gly Val Met Thr Gly Glu Ser Thr Ala Gly Val Met Ile Ser Leu
297 145          150          155          160
299 agc cgc atc ctc acg aag ctg ctg ctg ccc gac gag cgc gcc agc acg      528
300 Ser Arg Ile Leu Thr Lys Leu Leu Leu Pro Asp Glu Arg Ala Ser Thr
301          165          170          175
303 ctc atc ttc ttc ctg gtg tcg gtg gcg ctg gag ctg ctg tgt ttc ctg      576
304 Leu Ile Phe Phe Leu Val Ser Val Ala Leu Glu Leu Leu Cys Phe Leu

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VERIFICATION SUMMARY

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Input Set : A:\seq listing.txt

Output Set: N:\CRF3\01152002\J023673.raw

L:14 M:270 C: Current Application Number differs. Replaced Current Application No

L:14 M:271 C: Current Filing Date differs. Replaced Current Filing Date